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LETTERS TO THE EDITOR

Helical Structure of Ventricular Anatomy by Diffusion Tensor Cardiac MR Tractography

It is widely accepted that myocardial fiber architecture plays a critical role in myocardial contractility and relaxation (1). However, there is a lack of consensus about the distribution of the myocardial fibers and their spatial arrangement in the left and right ventricles. An understanding of the cardiac architecture should benefit the ventricular functional assessment, left ventricular reconstructive surgery planning, or resynchronization therapy in heart failure. Researchers have proposed several conceptual models to describe the architecture of the heart, ranging from gross dissection to histological presentation. The cardiac mesh model (2) proposes that the myocytes are arranged longitudinally and radially change their angulation along the myocardial depth. By contrast, the helical ventricular myocardial model states that the ventricular myocardium is a continuous anatomical helical layout of myocardial fibers (1).

Diffusion tensor cardiac magnetic resonance (DT-CMR) provides a discrete measurement of the 3-dimensional (3D) arrangement of myocytes by the observation of local anisotropic diffusion of water molecules. This has enabled computational validation of the muscular structure of the heart. It has allowed the measurement of the whole cardiac architecture with acceptable resolution (300 μm $\times$ 300 μm $\times$ 1,000 μm) compared with the size of myocytes (50 to 100 μm long and 10 to 20 μm thick). In this correspondence, we introduce a multiscale tractographic visualization approach based on DT-CMR streamlining to decipher properties of the architectural organization of the heart.

Canine datasets used in this study come from the public library of the Johns Hopkins University (3). Each heart was placed in an acrylic container filled with Fomblin, a perfluoropolyether (Ausimont, Thorofare, New Jersey), which has a low dielectric effect and minimal magnetic resonance signal, thereby increasing contrast and eliminating unwanted susceptibility artifacts near the boundary of the heart. The long axis of the hearts was aligned with the z-axis of the scanner, and images acquired with a 4-element knee phased array coil on a 1.5-T GE CV/I MRI Scanner (GE Medical System, Waukesha, Wisconsin) using a 40-mT/m maximum gradient amplitude and a 150-T/m/s slew rate. Hearts were placed in the center of the coil, and 3D fast spin echo sequence was used to acquire diffusion images. The datasets were arranged in arrays of approximately 256 $\times$ 256 $\times$ 108 voxels, wherein each voxel consisted of 3 eigenvalues and 3 eigenvectors; the size of each voxel was 312.5 $\times$ 312.5 $\times$ 800 μm. Tractography was performed as a reconstruction comprising several streamlines (4) (i.e., a curve tangential to the vectorial field of primary eigenvectors given at the diffusion tensor volumes) using a fifth-order Runge-Kutta-Fehlbert integration method (5). Our full-scale reconstruction was built with close to 350 seeds; these seeds were randomly chosen over the entire anatomy only taking out a very small range of points related to the lowest eigenvalues that are likely to be bad starting points for the reconstruction. The basal ring and atrial cavities were always included for reconstruction. Tractography is a graphical representation inherited from fluid mechanics in which both direction and orientation of the vector fields are a meaningful part of the represented information. We applied a geometrical reorganization of the vector field using local coordinate systems coherent with ventricular anatomy and fluid mechanics. Ventricular anatomy could be described by means of a longitudinal axis and angular coordinates with respect to this axis on axial cuts (Fig. 1). Coloring techniques were based on axial and longitudinal angulations of fibers to help in the

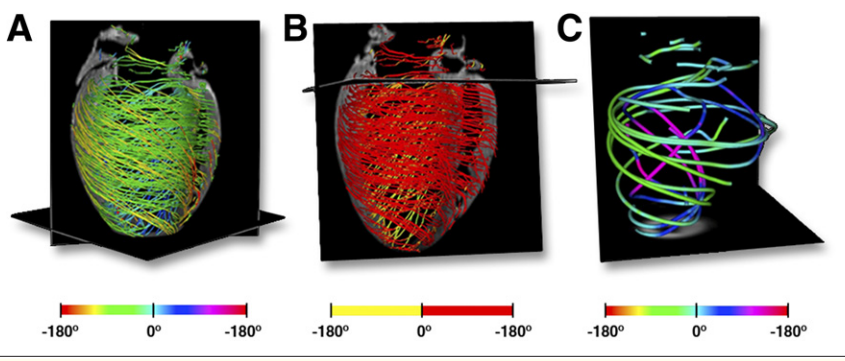

Figure 1. Results of Automated Tractography Reconstruction

(A) Tractography reconstruction with nearly 350 seeds, represented by a full-color scheme determining the orientation of the fibers. **(B)** Two-color scheme set increases the difference between counterdirectional helical fiber tracts. **(C)** Simplified tractography.

interpretation of the tractography models, which highlighted different features of the fiber architecture, adding valuable information of existent muscular layers. In order to further clarify the anatomic characterization, we applied multiresolution models that build different models of the same data with different levels of detail without losing fidelity. This technique is based on the well-known pyramid representation (6), which applies a Gaussian filtering and subsequent exponential reduction via a subsampling of the full-scale information. Reduced information is a summary of the original and would be used to represent it at different scales. This technique can be applied to the DT-CMR dataset in order to simplify its complexity. By downscaling 2 orders of magnitude of the original sets and applying our streamlining, we got a simplified tractography (Fig. 1). Comparing it to the full-scale tractography, also shown in Figure 1, it is easy to notice that the simplified one keeps the main geometric features of the fibers.

The simplified tractographic reconstruction method (Fig. 1) showed a continuous helical structure of the ventricular myocardium, tracked from the pulmonary artery (PA) to the aorta (Ao). The helical structure enclosing the basal ring can be further tracked inside the left ventricle toward the apex and is seen to orient in counterdirectional helical orientations around the ventricles. To further simplify the backbone myocardial fiber spatial orientation, we explored the geometry of the heart by looking for long paths that can represent connected regions on the DT-CMR tractography. The goal of this procedure was to provide a comprehensive reconstruction allowing interpretation at first sight by any possible observer. By manually picking seeds at the basal level, we resolved continuous paths connecting both ventricles. Figure 2 shows 4 tracts of simplified models reconstructed from manually picked seeds located at the basal level near the PA. We observe that the tracts define a sample-wide coherent helical structure for all canine samples. The use of visualizations with single tracts changes the way in which this structure can be viewed.

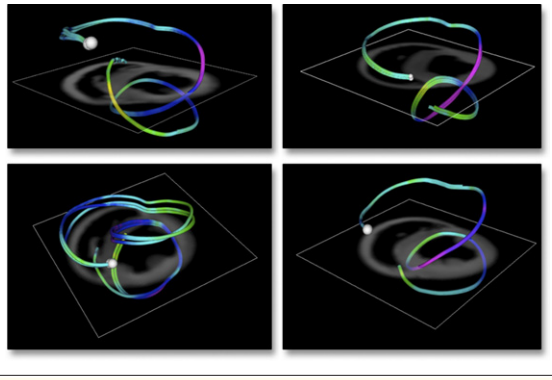

Figure 2. Selected Paths Highlighting the Helical Structure of the Myocardium

Example of tracts reconstructed with manually picked seeds, always chosen near the pulmonary artery, on simplified tractography.

Our reconstructions support a helical ventricular myocardial fiber array from a complete set of local evidence and also from a global automated reconstruction of the myocardial structure.

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Defining the Diagnosis in Echocardiographically Suspected Senile Systemic Amyloidosis

Senile systemic amyloidosis (SSA) is a cardiomyopathy mainly affecting elderly men due to intramyocardial deposition of wild-type (nonmutant) transthyretin (TTR) (1). Since the heart is the only involved organ, SSA—which requires endomyocardial biopsy (EMB) for a definite diagnosis—is often misdiagnosed as other, more common, causes of left ventricular "hypertrophy" (LVH), including hypertensive heart disease and hypertrophic cardiomyopathy (HCM) (1). We (2,3) and other groups (4,5) have previously documented that ^{99m}Tc-3,3-diphosphono-1,2-propanodicarboxylic acid (^{99m}Tc-DPD) has a high affinity for TTR-infiltrated myocardium (allowing a differential diagnosis with light-chain [AL] cardiac amyloidosis, in which the tracer uptake is low/absent) (2,3). However, the scintigraphic profiles of the non–amyloidotic cardiomyopathies potentially mimicking SSA are not known, and the